

IN THE CLAIMS:

The below listing of claims will replace all prior versions and listings of claims in the application.

1.-5. (Canceled)

6. (Original) A method of determining the lineage of an individual by analyzing genomic DNA in a biological sample of the individual, said method comprising:
analyzing said genomic DNA in said biological sample to determine the presence of a repeat sequence;
determining the repeat sequence's length in number of nucleic acids; and
comparing the repeat sequence's length with a corresponding repeat sequence length of a putative ancestor of said individual.

7. (Original) The method according to claim 6 wherein the analysis of said genomic DNA in said sample comprises using a first oligonucleotide primer for performing a first amplification on said genomic DNA, said first oligonucleotide primer being a 5' variation generator and comprising a repeat sequence and at least one non-repeat nucleotide on the first oligonucleotide's 5' end.

8. (Original) A kit of parts for analyzing genomic DNA in a sample, said kit of parts comprising:
first and second oligonucleotide primers for performance of a first nucleic acid amplification on said genomic DNA, said first oligonucleotide primer being a 5' variation generator, and comprising a repeat sequence and at least one non-repeat nucleotide on the first oligonucleotide's 5' end, and said second oligonucleotide primer being a 3' fragment generator.

9. (Original) The kit of parts of claim 8 further comprising:
third and fourth oligonucleotide primers, said third oligonucleotide primer comprising the oligonucleotide sequence of said first oligonucleotide primer together with further nucleotides, and said fourth oligonucleotide primer comprising the oligonucleotide sequence of said second oligonucleotide primers together with further nucleotides.\

10. (Original) The kit of parts of claim 8 further comprising at least one restriction enzyme.

11.-13. (Canceled)

14. (New) A method for determining the lineage of a subject, comprising:
acquiring a sample of the subject's genomic DNA including at least one genomic repeat sequence;
identifying the at least one genomic repeat sequence;
determining a length of the at least one genomic repeat sequence; and
comparing the length of the at least one genomic repeat sequence with a length of a corresponding repeat sequence of a putative relative of the subject.

15. (New) The method according to claim 14, wherein identifying the at least one genomic repeat sequence comprises:
providing a first oligonucleotide primer and a second oligonucleotide primer; and
conducting a first nucleic acid amplification on the subject's genomic DNA using the first oligonucleotide primer and the second oligonucleotide primer to produce amplified DNA fragments based on repeat sequences on at least one end of the subject's genomic DNA.

16. (New) The method according to claim 15, wherein providing the first oligonucleotide primer comprises providing an oligonucleotide primer including a repeat sequence and a non-repeat nucleotide located on the 5' end thereof, the non-repeat nucleotide serving to localize the first oligonucleotide primer to the 5' end of the at least one genomic repeat sequence.

17. (New) The method according to claim 15, wherein providing the second oligonucleotide primer comprises providing an oligonucleotide primer that starts within an amplification-permissive genetic distance on the 3' side of the at least one genomic repeat sequence.

18. (New) The method according to claim 15, wherein providing the second oligonucleotide primer comprises providing an oligonucleotide primer including at least one non-selective base.

19. (New) The method according to claim 15, wherein providing the second oligonucleotide primer comprises providing an oligonucleotide primer including at least one inosine residue.

20. (New) The method according to claim 15, further comprising:
providing a third oligonucleotide primer and a fourth oligonucleotide primer; and
conducting a second nucleic acid amplification using the third oligonucleotide primer and the fourth oligonucleotide primer on amplified DNA fragments produced by the first nucleic acid amplification to enable a selection of a sub-set of the amplified DNA fragments produced by the first nucleic acid amplification, wherein the third oligonucleotide primer is an elongated version of the first oligonucleotide primer and the fourth oligonucleotide primer is an elongated version of the second oligonucleotide primer.

21. (New) The method according to claim 20, wherein providing the fourth oligonucleotide primer comprises providing an oligonucleotide primer including at least one non-selective base.

22. (New) The method according to claim 20, wherein providing the fourth oligonucleotide primer comprises providing an oligonucleotide primer including at least one inosine residue.

23. (New) The method according to claim 15, further comprising digesting the products of the first nucleic acid amplification with a restriction enzyme to increase the number of genetic polymorphisms detectable in the subject's genomic DNA and to decrease the sizes of the amplified DNA fragments.

24. (New) The method according to claim 20, further comprising digesting the products of the second nucleic acid amplification with a restriction enzyme to increase the number of genetic polymorphisms detectable in the subject's genomic DNA and to decrease the sizes of the products of the second nucleic acid amplification.

25. (New) The method according to claim 15, wherein conducting the first nucleic acid amplification comprises conducting a polymerase chain reaction amplification.

26. (New) The method according to claim 20, wherein conducting the second nucleic acid amplification comprises conducting a polymerase chain reaction amplification.

27. (New) The method according to claim 15, wherein conducting the first nucleic acid amplification comprises conducting the first nucleic acid amplification under stringent conditions.

28. (New) The method according to claim 20, wherein conducting the second nucleic acid amplification comprises conducting the second nucleic acid amplification under stringent conditions.

29. (New) The method according to claim 20, further comprising diluting the products of the first nucleic acid amplification before conducting the second nucleic acid amplification.

30. (New) The method according to claim 15, wherein providing the first oligonucleotide primer comprises providing an oligonucleotide primer selected from the group consisting of SEQ ID NOS: 3-10.

31. (New) The method according to claim 15, wherein providing the second oligonucleotide primer comprises providing an oligonucleotide primer selected from the group consisting of SEQ ID NOS: 11-15.

32. (New) The method according to claim 20, wherein providing the third oligonucleotide primer comprises providing an oligonucleotide primer selected from the group consisting of SEQ ID NOS: 16-21.

33. (New) The method according to claim 20, wherein providing the fourth oligonucleotide primer comprises providing an oligonucleotide primer selected from the group consisting of SEQ ID NOS: 22-27.

34. (New) The method according to claim 14, wherein the putative relative of the subject is a putative parent of the subject.

35. (New) A kit of parts for conducting a first nucleic acid amplification on a subject's genomic DNA that includes at least one genomic repeat sequence, comprising a first oligonucleotide primer including a non-repeat nucleotide located on the 5' end thereof and a repeat sequence, the non-repeat nucleotide serving to localize the first oligonucleotide primer to a 5' end of the at least one genomic repeat sequence; and a second oligonucleotide primer that starts within an amplification-permissive genetic distance on the 3' side of the genomic repeat sequence.

36. (New) The kit of parts of claim 35, further comprising the following parts for conducting a second nucleic acid amplification on the products of the first nucleic acid amplification:

a third oligonucleotide primer comprising the sequence of the first oligonucleotide primer together with additional nucleotides; and
a fourth oligonucleotide primer comprising the sequence of the second oligonucleotide primer together with additional nucleotides.

37. (New) The kit of parts of claim 35, wherein the second oligonucleotide primer further comprises at least one non-selective base.

38. (New) The kit of parts of claim 35, wherein the second oligonucleotide primer further comprises at least one inosine residue.

39. (New) The kit of parts of claim 35, further comprising at least one restriction enzyme.

40. (New) The kit of parts of claim 36, further comprising at least one restriction enzyme.

41. (New) The kit of parts of claim 36, wherein at least one of the additional nucleotides of the fourth oligonucleotide primer is a non-selective base.

42. (New) The kit of parts of claim 36, wherein at least one of the additional nucleotides of the fourth oligonucleotide primer is an inosine residue.

43. (New) The kit of parts of claim 35, wherein the first oligonucleotide primer is selected from the group consisting of SEQ ID NOS: 3-10.

44. (New) The kit of parts of claim 35, wherein the second oligonucleotide primer is selected from the group consisting of SEQ ID NOS: 11-15.

45. (New) The kit of parts of claim 36, wherein the third oligonucleotide primer is selected from the group consisting of SEQ ID NOS: 16-21.

46. (New) The kit of parts of claim 36, wherein the fourth oligonucleotide primer is selected from the group consisting of SEQ ID NOS: 22-27.